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Post-processing: Minimum Match 0%
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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AUTHORS
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KEYWORDS
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PATENT: WO 9906567-A 11-FEB-1999;
LUBITZ WERNER (AT); RESCH STEPHANIE
LOCATION/Qualifiers
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SECRETION OF CARRIER-BONDED PROTEINS
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/translation="MDRKKAVKLATASAIAASAFYAANPNASEAATDVATYVSQAKAQ FKKAYYTYSHTVTETGEFNINDYAEYJKKAKKXYRDAVALDKAKAGGAKDAYLADLQ KEYETYVFKANPKSGEARVATYIDAYNATAYNATAKAGHARAGAYADLAYAGYYKI PYEIKTTYTDLLRSTFKAKAQELRDSLIYDITVAMKAREVQDAVKAG NLDKAKAAAVDQINQYLPKVTDAFKTEITEVAKKALDADEAALTPKVESVSAINTQNKA
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ALO31744 Plasmodiu
ACO23334 Homo sapi
X53237 D. discoide
X95661 M. hominis 1
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ACO06278 Plasmodiu
X01094 Trypanosoma
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ACO20602 Homo sapi
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Z33043 M.capricolu
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166494 Sequence 14
AF270648 Plasmodiu
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Y18528 Plasmodium
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1500 1500	actgcaaacgcatcagcaccaactgttgctaccgctcctactactttaggtggtacaact	y 1441 b 1441	D 6
1440 1440	gctatcaataatgttaaaacattaactggttacaatgcagaagcttacgagttagtgttc 	y 1381 b 1381	dd Vo
1380 1380	ggttctacaattactattacgttaaaagaagcgttagtagctggtaaacaatataaactt	y 1321 b 1321	g So
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1260 1260	acagtagtatttgataagttgttagcacctgaaactgtaaacagctcg 	y 1201 b 1201	<u> </u>
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1140 1140	gatgcattcactttcaagcttcgaaatgatgctgtagttactcaagtg 	λλ 1081 γν 1081	β δ
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840	. actccaaaagttgaaagtgtaagtgcgattaacactcaaaacaaagctgttgaattaaca	y 781 b 781	β δ
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2940	81 gtattcactccatctcaagaattaaaagctggtacagtttactctgtaacaattgacggt	, 281	S S
2880	21 GCAGCAGGTAATGCGGTAGCTGGTACTGTAACAGCATTAGACGGTTCTACAAATAAAT	28	맖
2880	cagcaggtaatgcggtagctggtactgtaacagcattagacggttctacaaataaat	28	Ϋ́O
2820	TTCAATGAAACTGATTTAGCGGAAGTTAAACCTGAGAACATCGTTGATAAAGA	27	뫄
2820	ttgaattcaatgaaactgatttagcggaagttaaacct	27	δŌ
2760	01 CAAAACGCTTCTGCTGCATTCCCAACAAGCACTGCAATTGATACAACTAAGAGCTTATTA	27	맖
2760	aaaacgcttctgctgcattccccaacaagcactgcaattgatacaactaagagcttatt	27	Qy
2700	41 CGTTACAACA9CTGGAGACACACTGTAGCTTCTGTGAAAGCTGCTGCTGACAAAGA	26	닭
2700	gttacaacayctggagacacactgtagcttctgtgaaagctgctgctgacaaagatgg	26	γo
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2580		25	뫄
2580	21 ttaactggtcttgacaataacgacaaagatgcgaaattgcgtctggtagtagataagtc	25	δĀ
2520	61 ACTGTATCAGTTGCTCCTAAGACAGATGCAAATGGTAAAGTAACAGCTGCTGTGGTTACA	24	뒩
2520	ctytatcayttyctcctaagacagatgcaaatggtaaagtaacagctgctgtggttac	24	δ
2460	AACTGTCGAGAAATTAACAAACAACGGATGGGTAGATGCTGGTACTGGAA	24	슔
2460	gcaaagtaactgtcgagaaattaacaaacaacgatgggtagatgctggtactggaac	24	γQ
2400	41 CAAAAATTCACTATCCAATTTAGCGAAGAATTAAAAACTTCTAGTGGTTCTTTAGTGGGT	23	Db
2400	aaaaattcactatccaatttagcgaagaattaaaaacttctagtggttctttagtggg	, 23,	Š
2340	81 AAAGGTGATTCTTTAAAAGACGCTGATGCAGTTACTACACTTACGAACGTTGATGCAGGT	22	망
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2280	21 ATCTATACATTTACAACTGAAGGTCAAGACGTAACAGCACCAACGGTTACAAAAGTATTC	22	뮸
2280	tctatacatttacaactgaaggtcaagacgtaacagcaccaacggttacaaaagtatt	22	γQ
2220	61 AAAGGTGCAACAGCTCCTGTTAAAGATGCTGCAAATACTTTAGCAACTAT	21	뮍
2220	aaggtgcaacagctcctgttaaagatgctgcaaatgcaaatactttagcaactaact	21	γΩ
2160	01 GTGAAAGTTGCTGCTAACCAATTAGAACGTAACCAAGGGTACAAATTAGTAGTGTTCGGT	21	닭
2160	tyaaagttgctgctaaccaattagaacgtaaccaagggtacaaattagtagtgttcgg	21	δō
2100	41 GCAAGTGACATCCAGCTAGTGTTGAAGCGGTTACTGGTCAAGATGGAACATACAAA	20	닭
2100	41 gcaagtgacatcattccagctagtgttgaagcggttactggtcaagatggaacatacaa	, 20,	Qy Qy
2040	81 ACAATCACATACGGTCAAGTTGCTGTAGTAAAAGCGGGTGCAAACTTATCTGCTCTTACA	19	뮍
2040	caatcacatscggtcaagttgctgtagtaaaagcgggtgcaaacttatctgctcttac	, 191	£Ğ
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1920	61 GTTATTAGCGTAACGTCTAAAAATGGCGACGCTGGATTAAAAGTAACTGAAGCTCAAGAA	) 18	닭
1920	ttattagcgtaacgtctaaaaatggcgacgctggattaaaagtaactgaagctcaag	, 18	ξŌ
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1860	taggcactgttaacgagaaaacatatgagttcaaaactcaagacttaactgctcctac	. 18	γQ

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Lubitz,W. and Sleytt,U.
RECOMBINANT EXPRESSION OF S-LAYER PROTEINS
Patent: WO 9728263-A 07-AUG-1997;
LUBITZ WERNER (AT); SLEYER UWE (AT)
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Kuen,B., Sleytr,U.B. and Lubitz,W.
Sequence analysis of the sbsh gene encoding the 130-kDa surface-layer protein of Bacillus stearothermophilus str Gene 145 (1), 115-120 (1994)
94320770
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Bacillus stearothermophilus
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Bacteria; Firmicutes; Bacillus/Clostridium
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AF055578
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Jarosch,M., Egelseer,E.M., Mattanovich,D., Sleytr,U.B. and S. S-layer gene sbsC of Bacillus stearothermophilus ATCC 12980: molecular characterization and heterologous expression in
                                                                                                                                                                                                                                                                                                                                                                                             AF055578 3680 bp DNA
Bacillus stearothermophilus
gene, complete cds.
                                             Sequence update by submitter on Apr 13, 1999 this sequence Location/Qualifiers
                                                                                            Submitted (13-APR-1999) Zentrum Universitaet fuer Bodenkultur, G
                                                                                                                                                                               Direct Submission
Submitted (25-MAR-1998)
                                                                                Vienna, Austria
                                                                                                                    Jarosch, M., Egelseer, E.M., Direct Submission
                                                                                                                                                        Universitaet fuer Bodenkultur,
Vienna, Austria
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YKTFTVEAADLSVAADKTGFTATVTPTGGNQVTTGKTLLAVSDLANGHKLYAAAAGSS
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Bacillus stearothermophilus
Bacteria: Firmicutes; Bacillus/
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Molecular characterization of the first bacterial S-layer
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19-APR-1994 JP 1994080643
                                                                    AGAAGAAGAAAAGTAACACATGAAGAAGAAGAAAAAAGTAACATATGAAGAAGAAGAAGA
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/strain="shizuoka"
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"GENE CLONE MANIFESTING CHICKEN LEUCOCYTOZOON IMMUNOGENIC RECCOMBINANT VACCINE AGAINST CHICKEN LEUCOCYTOZOON";
Patent number JP 1995284392-A/2, 31-OCT-1995.
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    DNA encoding an maltose-binding
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31-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=FID9
Genes with similarity to proteins in the databases are described 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://cCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and Genes (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical University of California (S.M. Hebsgaard, et al., CBS, Technical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicePredictor (Volker Brendel, Stanford University, http://grenlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (strain:Columbia)
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                                                                                                                                                                                                                                                                                                                                                                                             clone is T8N9 and the 3' clone is T7B9.
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BAC clone:F1D9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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PGIKIITLETLVSKSSKLGIKDKLIIIIVVIVKLVMP"
Join(21817...22004,22075...22143)
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gb|AAC97228.1
gene_id:F1D9.3"
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/evidence=not_experimental
/evidence=not_experimental
/product="helicase-like protein"
/oin(11589. .11736,11836. .12019,12305. .12497,12774. .12896,
/13021. .13080)
/note="gene_id:FlD9.2"
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/note="gene_id:FID9.1"
                                                                                                                                        strong similarity
                                                                                                                                                                                                                                                                /evidence=not_experimental
product="ATP-dependent CLPB protein-like"
join(40639 .40982,41779 .42326,42393 .43794,42903 .4
43020 .43142,43226 .43333,43425 .43481,43588 .43650,
43733 .43973,44026 .44107,44503 .44674,44813 .44940,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
complement(25073. .29379)
/note="gene_id:F1D9.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(24404. .24543,24659. .24879)
/note="contains similarity to ATP-dependent CLPB protein
gene_id:FID9.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains similarity to
gene_id:F1D9.4"
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                                                                                                                                                                               gene_id:F1D9.9
                                                                                                                                                                                                           45043. .45198)
/note="gb|AAD25852.1
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/evidence=not_experimental
complement(22489. .23812)
/fiote="contains similarity to
       /evidence-not_experimental
join(46889. .47780,47984. .48332,48695. .48783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="retroelement pol polyprotein-like"
join(30097..30190,30265..30551,30614..31510,31758..32036)
/note="gene_id:F1D9.8"
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/note="gb|AAD23008.1
                                                                                                  strong similarity to
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gene_id:F1D9.13"
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/protein_id="BAB01984.1"
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/pseudo
/evidence=not_experimental
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/translation="MLSKVKIPLPDLMSSVLALDESVIDVDQVDNLIKFCPTKEEAEL
LKGFIGNKETLGRCEQFFLELLKVPRVETKLRVFSFKLOFHSQVRGSTKLKRHOTIL
SLGNALNHGTARGSAIGFHLDSLLKLTDTRSRNSKMTLMCLKGVLAEKLPGLNFP
KDMIQLKYLAEEMQATSKGLEKVVQETTASETDCQISKHFHMNLKEFLSVAEGEVRSL
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complement(join(81294 .81521,81620 .82285))
/note="gb|AAD23008.1
gene_id:F1D9.18
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/evidence=not_experimental
join(51111. .51234,51470. .52398,52474. .52672,52762. .5
.53433. .53558,53717. .53809,53908. .54010,54110. .54210,
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.55334. .56637,57320. .57389,57601. .58187)
/note="gene_1d:F1D9.11
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/product="maize transposon MuDR protein-like"
/product="maize transposon MuDR protein-l
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RESULT
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ORGANISM
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                                                                                       malaria parasite P. falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplo
                                                                                                                                                                    antigen gene, complete AF056936
                                                                                                                                                                                       AF056936 5420 bp DNA DNA Plasmodium falciparum mature parasite-infected
   92158014
                                            Repeat structures in a Plasmodium falciparum protein
                                                                                                                                                      AF056936.1
              inds human erythrocyte protein 4.1
ol. Biochem. Parasitol. 50 (2), 335-347 (1992)
                                                                            (bases 1 to 5420)
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88953. .89075,89158. .89715))
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44.38;
                                                                                                                                                      GI:3044184
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Pred. No.
                                                                                         Apicomplexa; Haemosporida;
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                                                                                           Plasmodium.
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                 aagacgcttacttagctgatttacaaaaagaatatgaaacttacgttttcaaagcaaacc 340
                                                                               aagcgaaaaaacgataccgtgatgcggtagcattagtgaataaagcaggtggcgcgaaaa 280
                                                                                                                       ACAAAGATAALGAGATAGAACAAGAAAAAGAAAAGAAGAAGTTAAAGAAAAAGAAGC 2885
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Conservative

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Score 73; DB 33; I Pred. No. 0.0069; 0; Mismatches 530;

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2 (bases 1 to 5420)
Kun,J.F.J., Waller,K.L. and Coppel,R.L.
Plasmodium falciparum: Structural and functional domains of the
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1, J.F.J. and Coppel, R.L.
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                                                                                                                                                                                                /db_xref="taxon:5833"
join(<1. .150,281. .>5116)
/product="mature parasite-infected erythrocyte"/
/product="mature parasite"/
/product="m
                                                                                                NVVHQILNYEERIRMYEENAARGRLNTVILDPIITFNVIFGDDTMFKFIDE"
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                                                                                                                                                                                                                    Homo sapiens chromosome 6 clone SEQUENCE, 12 unordered pieces. AC024253
 2 (bases 1 to 179553) Waterston, R.H. Direct Submission
                                                                                                 The sequence of Homo sapiens clone Unpublished
                                                                                      Waterston, R.H.
                                                                                                                                                                                      AC024253.3 GI:8568958
HTG; HTGS_PHASE1; HTGS_DRAFT
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RP11-758C19,
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Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of 1
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 198000; agarose-fp
Insert size: 178453; sum-of-contigs
Quality coverage: 4477.53 in Q20 bases; agarose-fp
Quality coverage: 4.99 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 175235 bases at least Q40 Consensus quality: 176522 bases at least Q30 Consensus quality: 177171 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7235339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Center code: WUGSC
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/note="assembly_name:Contig8
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 /note="assembly_name:Contig9"
16535. .24088
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43110. 52414
/note-"assembly_name:Contig13"
52515. 78544
/note-"assembly_name:Contig14"
78645. 107099
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24189. .32883
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37751 c 36838 g 54991 t
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sequence comes from fig1b.
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TEVTVDNRTILLTWMHLLCESETELDKSVFPLSVSILDRYLCKKOGTKKILOKIGAACV
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NALKIPEDLMPQLYEAASTTICKALIQPNIALLSPGLICAGGLLTTIETDNTNCRPWT
                                                                                                                                              ./note="G protein-coupled
.2726. .3691
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                                                                                                                                                                                                                                                                                                complement(1004. .2227)
/gene="ORF 5' of ECRF3"
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/gene="ORF 5' of ECRF3"
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ETLSKSTQWDICLMQCL"
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                                                                                                     /codon_start•
                                                                                                                                                                                         /gene-"ECRF3"
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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                                                                                                                                                                                          Nicholas, J., Cameron, K.R., Coleman, H., Newman, C. and Honess, R.W. Analysis of nucleotide sequence of the rightmost 43 kbp of Herpesvirus saimiri (HVS) L-DNA: General conservation of genetic organization between HVS and Epstien-B arr virus
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                                                                complement(1. .409)
                                                                                              /organism="Saimiriine herpesvirus
/strain="11"
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/EC_number="3.6.1.2
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NILCEWLDKTDSELSTYLAGEIPKLTVLKYPTHEKVCEPTIPMORWCLHNLLGIEQY
YKDESNIVLHDPETSLGSVQAYSRLSKLLFWCDSFMNKIYPCNAFNSSINOVULMSTW
FHFYSVAHCNDCISESISFTEALLKQEYSAFYEWCLEEEYEEDRMAKFMKFSADQITI
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LRRFFLRNDLGFLSAVVILKQYVENLFTTKQKLNLIECTQGLKFLIRSLYEKIKDQCD
VKSSIREIFYDCKARLLLLLEEGCGCGACCATSA"
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/db_xref="GI:339982"
/tanslation="MYMENEFICELSPGVIFLRVSSLTEKSHTTSYTILHNNNFYSNSC
SADTYYPSIKTFSSVWAILNVIIFFCASLFYLRHLCIVKFISNLTK"
                                                                                                                                                                                                                     complement (4549
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="EDLE3 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLNSTPNKPLSSTKLTPKSQSSSQSTKTTKQASKNLTTSKLATSFSSTYMTTSDQPYS
NNTANKILLNTTYIYLSTLSKITKLFMQEQNKTTQEPFELITPSSTERDSSTLSKHTN
KLKPFKPKTQPIVNMQRTWIYPLTGIVSIVVLLIIMSCIHCYIRREDEHFE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAÂ46128.1"
/db_xref="G1:339980"
/tabslation="MKAQALLLCSLYLLAQSTDVDDEGSGEVFLQXVSSSVSITASLA
TTMLTSVTNKTTQNVSVTTIDSLSTSPMHNATSNTSYSQTTPYSQTSLSSSVLISTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="noripiwivrsthclillfoddvqvrksclepflfisperkrei
HOLLVAFNQSLVTPTQDEEKILSDIQRACLQIAEDLKHLNPFTGLLLDLNLYTLMTLL
RNYKTKQRSQPVNSTVVSRYAHHVVKYIMQRLVYTTDRLFLTAPTSGIYLPVPLANAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="transactivator"
/protein_id="AAA46124.1"
/db_xref="GI:330979"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSTHTDLQNLAEYIYSYKKCLINRRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA46127.1"
/db_xref="GI:330978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(604..609)
                                                                                                                                                                                                                                            NLSRRPASKPRTK"
                                                                                                                                                                                                                                                                                                     /protein_id="AAA46129.1"
/db_xref="G1:330981"
/translation="MASRRSCADVEELEKELQKLKIENKALKKKLVQHTSPEDELLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="5' end of coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=:
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                                                                                                                                                                     complement(4550.
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="first methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="EDRF2 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="EDRF1 ORF"
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                                                                                                                                                                                            /note="EDLF2 ORF"
                                                                                                                                                                                                                                                                              AQKDAIINSTVNKLTKKAEEKIRERVLKDVLPLVSKNQCMEAIAHIKYRIDVSIDETY
                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MSRPYQPQRYSLISELHKNFHYVDVSVIQSEFKNVILKTVVPKL/
                                                                                                                                     note="first methionine codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transpressor"
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                                                                                                                                                                     .4822)
                                                                                                                                                                                                                     .4554)
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                                                                                                                                                                                                                                                                                                                                                                                                                    codon
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codon

in the EDRF3 ORF'

5'-triphosphate

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polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mmeateampkfkvlfatdgdsaeiitdiltgtdtnafiysvlhn
cyiyptevkivliclpakkpgggdkcleveqlhidytelaiptfletytkplkandlhky
idfkaarknekpildiistnkpspkthusdikskipekkkevnslkkkykissspym
mittegsfevpelltaltyffedholtistnitiellegkklotslaittfeelggv
cstsdylktapafinychiklardslesgaidtsidtlrglalsngdluhyiylsff
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cihlpdligyapodctsfyymaggskuhnllnviltphhnisedlnglldhahid
stenvunkrdevferskypyrgefikktsrhetypvrlydnilknymstdvlhelmfishei
stenvunkrdevferskypyrgefikktsrhetypvrlydnilknymstdvlhelmfishei
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IEACPFVLFIGMGVFALKNIFHEHPVFFNILITCKPIFTAKNKYKTKGTEVNMKLVVHN
IEACPFVLFIGMGVFALKNIFHEHPVFFNILITCKPIFTAKNKYKTKGTEVNMKLVVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="transactivator"
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WADRVVEBAAAQRRPSRPFRKFYSHPRNOPLRNCPPRAPPLKLFDISILPKSGEPKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="EDRF4 ORF"
complement(9074. .9079)
/note="EELF5 ORF"
<9082. .10320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA46132.1"
/db_xref="G1:330984"
/td_xref="G1:330984"
/translation="McMuHSCWPFGKYRRQKYVPLDTSSSCPDRWKIEIEIAQPPGV
FVGDIIQNSDSDASLRQAYLLAVQLNNITDYLKRFDEASVPESCKSVVQTQITKLKSV
RNIIWNTMLSMAVGGYTIDDAALKTLLDKRAGESIALIEMEKLATAIVMDDSKAWAKE
                                                                                                                                                                                                                                                                                                                                                                                   LPVPSLPCQEAEKTNDKYVLAMAQRAMHDVPISSKQLTANLLPVKFKPLLSIVRYTPN
YYYWVSMRKETIASANLCTVAAFLDESLCWGQQYLKNDFIFSENGKDIILDTSSALLS
QLVHKIKMLPFCHCLMQTTPQDHIVKQVCYLIASNNRILDAVRYLQTSVIKSPIVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGFRIITPLPAGVVLLGSNPVISFVNILNRTIKIDKKLLAMYPLIMETDGPFDVGIYH
KGRCVRIPATKVNSSGRLERLLKLFVCHENTDKLQYWDGSDINNLLYHSHNPEKV
KQLKAVYDIADTNENEILDKAQAQLFOQTHHNAVERIESASHMSTTDWYAEFAWPBLFE
LIKLYLSEEKVSQFYHVSFAASTGNIKIISLSGNFSCLNFKHRLKTQSVRIFLSLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPYKVPETYYREEPQTFYTTSPARASNLOLINHNNILVRAGQVT
IVSTGIIFPKETSFAFIILYGKSAKSIFCHTGLIDPGFQGELKLIVLNKTEDDITILFEN
DLRUSVTAFVYGVPKLHDYSDLCPPKYSKDAGFDLYLLFTDVTVKPRVPMYKSVNICCP
AQLKSYKPVLFGRSGLAAKGLTIKVSRWQNQLQIIFYNYTKSQITYTARTRIAQVVFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="EDLF1 ORF" complement(5797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5793
LGAVLFLLAVEFASVVSVVQRLDIFVGMQNYLFLLFVSMLCCCMFSLPSNAICVVLET
                                                                                                                                                                                                                                                  complement(10679.
                                                                                                                                                                                                                                                                                                                                  TRAIVGTKANTTGLFFLPTQ
                                                                                                                                                                                                                                                                                                                                                         AYAVCLPAAIICTKNETQLYSHCMRILKEYRPGDVMNILHESLTQHLNKCPSSTCAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPDNCVTLTLMSQCFASKCNSNKCIAHMSVRVPITDK"
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                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                   /note="first methionine
                                                                                                                                                                                                                                                                            note-"EJRF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="5' end of coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA46133.1"
/db_xref="GI:330985"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INNIILSAEHEKQILVNSEVPLIECETLAAEKTTTPAVSI"
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/note="first methionine"
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/db_xref="GI:330983"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'codon_start•1
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                                                                                                                                                                                                                                                                                                         .10430
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VERSION
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Best Local Sim
Matches 211;
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                                                                                                                                                                                                                                                                                                                           gctgttcaagcaaaagatttagaaaaaagcagaacaa 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaaaaaagctgtgaaactagcaacagcaagtgctattgcagcaagtgcatttgtcgctgca 69
                                                                                                                                                                                                                                                                                          GAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAA 37228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGCTGAAGAAGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCAAGAAGCT 37384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGCTGAAGAAGCTGAAGAAGAAGAAGCTGAAGAAGCTGAAGAAGCAGAAGAAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aacattaacgatgtatatgctgaatacaacaaagcgaaaaaacgataccgtgatgcggta 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGCTGAAGAAGCAGAAGCTGAAGAAGAAGAAGCTGAAGAAGAAGCTGAAGAAGAA 37504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cagttcaaaaaagcatactatacttacagccatacagtaacggaaactggtgaattccca 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGAAAAAGGAAGCTGAAGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                 tacatcyatycttacaactatycaacaaattagacgaaatycyccaagagctagagyct 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGAAGGAGAAGGAGGAAGAAGGAAGGAAGAAGAAGCTGAAGAAGAAGAAGCT
complete coding region.
Saimiriine herpesvirus 2
Saimiriine herpesvirus 2
Viruses; dsDNA viruses,
                                                                                                                        Herpesvirus saimiri
X64346
                                                                                               X64346.1
                                                                                                                                                                     HSGEND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(11774. .11779)
/note="EELF3 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MADTQTTHESYGVGFKPCVLQEHTKIYNHIKAVKDGIIQIEGL
TSSPSLRIWSSIGEGILSFKINNVVSEVFNCHMMPENVSVSFRNISPGGNTFLYTREL
FGCNVKTATLMFSNRSGKPFEFIKAKLEYCDKVSTTRHTSTIPAGILPFVENVNSTSV
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                                                                                            GI:60320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (12966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(11774. .11779)
/note="EELF2 ORF"
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LCNNPSKDWGVVQNDVQTKVNITALSAALGLCKIPGVFVPCIKFYESEVLEVCGTPVK
LGSWVDTSLQVTLFCTPNLAEDTQAAVSDYFPISPSACLTADPADTQEEPTLSSNCQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="required for DNA replication"
/product="DNA-binding protein"
/protein_id="AAA46135.1"
/db_xref="GI:330988"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(11749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="ribonucleotide reductase beta subunit"
/EC_number="1.17.4.1"
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                                                                                                                                                                          112930
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                                                                                                                                              complete
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Pred. No.
                           NN
  no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .13883)
                                                                                                                                              genome DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Albrecht, J.C., Nicholas, J., Biller, D., Cameron, K.R., Biesinger, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Albrecht,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92333688
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                                                                                                           KNSRLAISMNIDYMNPWSSTNMLYDGLHAIEKGLIYSFGSFTFTPSLTSVFNMAQHWY
VPMFSACQIGHYMQLPLQTHELSITGSLDMKMLQAHLMLLKCSSMPHIGGFFRLVPKD
LSHILPQTK IYNGFISISLCLQTINMANEHPLDDKTTLYLQCAWFFTYHKQFEFSISLCLQTINMANEHPLDDKTTLYLQCAWFFTYHKQFEFSISLCLQTINMANEHPLDDKTTLYLDDKTLAVICAQALKTACYMAGC
KEIGSILTALAFFLDSVKTYPGTIYGMSTSLPVASMKAKLAAVCQQVCGARLLVSALP
PQVVAKLAPFSDSNRVENKKMLKQYFFHLLFTSLTIAIKNVNLIDAQAALKTACYMAGC
RFKKIGLLTHLKGTEVVDUTVERPYPTLHFDBKRFKPFLLSSFTSIFELERINMQDL
NLRDTILKILLEHFSVGCKEFIVNHTDKLISGRVARTSIVGPMQLDVSDYSILVPMHPC
TTEEVRENFMYYETDLDSHCVETEAAVAGICSAIGESTILTQALKVSCTTANATEG
GASIVASAIVHTLDVSKCITIPDTKFNNSFLFLLTTEKDYSLFGSVAQQILEKTITGE
GASIVASAIVHTLDVSKCITIPDTKFNNSFLFLLTTEKDYSLFGSVAQQILEKTTIGET
GSATSFYMLKKHLSVLQTLIKDESVVSGHDVSDGGLVAITVAEHALSGGKGVRYVPHG
GSATIVATGATGTGATGTTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA45625.1"
/db_xref="G1:60323"
/db_xref="SG1:60323"
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/db_xref="SG1:6032"
/db_xref="SG1:603
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/gene="DHFR"
complement(3969. .4532)
SVPHGLLNAIEEAGFQPRLVSIHQPSKTTNVYDPHTVWGFFIVGASNVQDEDVGMRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mvoalncivavaonmgigkognlpwprlmndpkhformtitssv
pdkonlvimgkktwfsipeknrplkgrinvvlskelkelphrahflakslddalklte
opelankvdmvwiiggssvykeamsypcdlklfvtrimodfecotffpefdlekykll
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/translation="MARGLGEOPQENDESNGDPPHNTDERSDGDDGPTPYLPVTLLN
AGPFGPYNPYCLLGHHYQESGCPGRPTALSGAVGLPTPSGSRSSSHLSTPVGLSAVRV
SGCGGAGSEEHVYAEVGSLHSEHEQEGDKCTDCSVTILLLLVIIVLLLIIIGLMLVIM
                                                                               EDAIKFLCSETPGVVIEVQGSKMYYVQQFLHSENINFQIIGESTSSLTFSISQNLTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity to ORF 75 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKKK
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/gene="STP-A11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="dihydrofolate reductase"
/protein_id="CAA45624.1"
/db_xref="GI:60322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(220. .714)
/gene="STP-A11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYPSVLSNVQEEKSIKYKFEVYEKNH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SWISS-PROT:P09503"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ORF 02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"DHFR"
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/product-"saimiri transformation-associated protein."
/protein_id="CAM-5623.1"
/db_xref-"GI:60321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Saimirline herpesvirus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 map-"1-112930 nucleotide number"
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/gene.*'sCCPH*
10912. .1100.
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YVEVRKSATSWQYLHINVKCYKGFMLYGETPNTCNHGVWSPAIPECMKISSPKGDMPG
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SRKFESRWSNIYIPESTKAIAFQSLKNSLIPCWTQGTHLKFYHPKPMLEKMEESGMVS
SMFYGHSLSSGPAQNYPLTPNGENAIAGVCSADGRHLALLHDPSLCNNLWQWPYVPLE
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VKDFYTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLPQVANA
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VYTHLFSTNSVLYLTK INKQTQSNKSEQNVYNTYFMQHGLAYAADATQRENGEPAFSG
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INSNEDNSTPSGRICNGNCTTSMPTQTYTIITARYTSHIYFPTGKTYKLPRGVLVIIL
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/codon_start=1
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CDS

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Db 106810
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Best Local S
Matches 211
                                                                                                    106750 GAAGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCA
                                                                                                                                                                                                                                                                                                                                                                    106870 GAAGCTGAAGAAGCAGAAGCTGAAGAAGAAGAAGCTGAAGAAGAAGCTGAAGAAGAA 106811
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gaatatgaaacttacgttttcaaagcaaaccctaaatctggcgaagctcgtgtagcaact
                                                                                                                                                                                                                                    GAAGCTGAAGAAGCTGAAGAAGAAGAAGCTGAAGAAGCTGAAGAAGAAGCTGAAGAAGAA 106751
                                                                                                                                                                                                                                                                                    aacattaacgatgtatatgctgaatacaacaaagcgaaaaaaacgataccgtgatgcggta
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                                                                                                                                                               cagttcaaaaaagcatactatacttacagccatacagtaacggaaactggtgaattccca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGAAGGAGAAGGAGAAGAAGGAAGGAAGAAGAAGCTGAAGAAGAAGAAGCT 106931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLRGVSPIPLPDTYLSNIPCIYCLNEHMMLPNQGESLPSLMMCVNCKHVCKQLNPEPI

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LSKITLQFYKLITGPLSQNVSFFPLPSNIALAHCLDAAGALPHKKLLTUFSALNFEK
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IYLQIMPLLHKQNNIESTSLSVELQHLLHNLKIVLETFSAHLSDYNMYFENIHSLSAP
CSRHKSIVFOFYNNCCYSVKMCIINDIBIFSKKLSSVFYCIRSCDALRGINHVIDFLG
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DNVDSEVVKFMNCLVKNNINFRETIKTVHHVLHYCCNVFWQAPCAMELKLEYKSVLA
IIQDICLFIAMTYEQDNBSIGMMPSEMLKVHYOTIWTWEKSSCLDRGVLTGSEHKIVH
TDMFCDFLNIDSALSGQIVPMKMQVRLAKALLTVPKTIKIKNRIVFSNSSMTETIQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGWTREGVAITNKWELSRAVPKYEIDIMDKTYOCHNCMOIEVNGMLNSYYDRDGNNKT
VDLKPVDGLIGAITRYISOPKVFADPGWLWGTYRTRTTVNCEIVDMFARSADPYTYFV
TALGDTVEVSPFCDVDNSCPNATDVLSVQIDLNHTVVDYGNRATSOOHKKRIFAHTLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCVNLSPNQFCSGIYLTYEDSSPLIFVYENQGWVFKDLYALLYHHLQLSGKNHGT"
18006. .20432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="glycoprotein B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L., Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J., Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O., Smith, H.O., Fraser, C.M., Hoffman, S.L. et, al. Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE001373 : 12029 bp DNA
Plasmodium falciparum chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erratum:[[published erratum appears in 4;282(5395):1827]]
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KSIONFENCYKKOSNOFPRSYPEFFEANFGPIDELMDETDYSSDDLEDQLNYGYRGIE
                                                                                                                                                                                                                                                                                                                                       EKKYMYQRIIVEREDVIWKQDFKITLNEKSYERLNLPTEKQIPYSTCSEEIEKVHNLT
TRVTEIWKLLLEQMEVKYLIKTDNMNHKWRDFMWESKWALYLENVYKFINDKLNEPHV
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                                                                                                                                                                       codon_start=1
                                                                                                                                                                                             note="predicted"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="PFB0110w"
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BASE COUNT ORIGIN Query Match 1.7%; Best Local Similarity 43.7%; Matches 336; Conservative Score 62.6; DB 32; Length 12029; Pred. No. 0.3; 0; Mismatches 424; Indels 9;

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멍 Ş 8037 184 GAATCAGAAAAAGATAAAGAAGAATCAGAAAAAGACAAAGAAAAAACTGAAGAAGATGAA 8096 ttcccaaacattaacgatgtatatgctgaatacaacaaagggaaaaaacgataccgtgat 243

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В Qy 밁 δ. 8157 8097 304 GAAAAAACTGAAGACGAAAAAGGAACGGAAGTATACAAAAAAGAAACAGATGTAGATGAA 8156 caaaaagaatatgaaacttacgttttcaaagcaaaccctaaatctggcgaagctcgtgta 363 

밁 δÃ 8217 364 GAAGACGAAGAAACAAAAGTAGAAGAAAAGAAAACAGAAA-----AAGACGAA gcaacttacatcgatgcttacaactatgcaacaaaattagacgaaatgcgccaagagcta 423 8267

В QΥ 8268 424 GAGGGAACAGATTATGAAGAAGATACAGATGATTCAGACAAAGATGAAGAAAAAAAGTA 8327 gaggctgctgttcaagcaaaagatttagaaaaagcagaacaatactatcacaaaattcct 483

В δÃ 484 tatgaaattaaaactcgcacagtcattttagatcgcgtatatggtaaaaccaactcgtgat 543

밁 δÃ 544 ttacttcgctctacatttaaagcaaaagcacaagaacttcgcgacagcttaatttatgat 603 GTAGAAAAAAAGAAAAACAGAAAAAAGACGAAGAAGAACAGATTATGAAGAAGATACAGAT 8447

δÃ 밁 8448 604 attaccgttgcaatgaaagcgcgcaagtacaagacgctgtgaaagcaggcaatttagac GATTCAGACAAAGATGTAGAAACAGAAGTAGAAGAACAGAACAGACGCAGAAGAACAAGAAGAA 663

Š 밁 Š 724 aaaactgaactaacagaagtagcgaaaaaagcattagatgcagatgaag 772 aaagctaaaagctgctgttgatcaaatcaatcaatacttaccaaaagtaacagatgctttc 723 AACGAAGAGGGAACAGATGATGAAGAAGACAAAGTAGAAGAAACAGACCTAGACGACCAA 856

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